

Germany, ⁴CAT Catalytic Center, RWTH-Aachen University, Aachen, Germany, ⁵IEAP, Christian-Albrechts-University of Kiel, Kiel, Germany. The lipid membrane matrix represents a 2-D liquid-crystal, the properties of which, at fixed other conditions, are locally modulated by the presence of effectors as e.g. cholesterol (passive) or proteins (passive and active). Not only does the incorporation of effectors into the host matrix locally or even globally modify the initial state of the host per se, most probably the state of the matrix in turn serves as a control tool for regulating the work of functional units (e.g. proteins). Results are presented on a membrane model system that was inoculated with a photosensitive and thus active variety of cholesterol. Azobenzene-cholesterol (azo-chole) exhibits a reversible trans-cis transition (365nm: trans- to cis-; 455nm: cis- to trans-). In a membrane, the azobenzene group, covalently connected to the cholesterol by an ester bond, is confined into the headgroup region. The system was explored by a combination of spectroscopic (UV-vis, NMR, mass spectroscopy), thermodynamic (Langmuir compression, calorimetry) and structural studies (X-ray/neutron reflectometry, grazing incidence X-ray diffraction). The conformational change of the guest upon illumination is coupled into the host system, inducing a transition of the whole membrane. The increased demand of headgroup area for the cis-azo-group pushes the membrane into a more compressed state, and vice versa for trans-azo-chole. The switching process between the two final states exhibits first-order kinetics. The state of the host bilayer is modulated as a response to the conformational switching of the guest effector via external light illumination. In a more general context, similar behavior may be found upon the conformational changes of membrane proteins during work.

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Creating Fluid Supported Lipid Bilayers with High Amounts of Phosphatidylethanolamine

Anne Sendeci, Matthew F. Poyton, Tinglu Yang, Paul S. Cremer. Chemistry, Pennsylvania State University, University Park, PA, USA. Phosphatidylethanolamine (PE) comprises 20-50% of overall phospholipid content in human cell membranes and constitutes 70-80% of the membranes in gram-negative bacteria. Its presence is specifically required for the proper folding of numerous membrane proteins, the function of active transport systems, cell division, fusion, blood coagulation, and may play a role in neurodegenerative diseases. Unfortunately, it is hard to work with this lipid in model systems like supported lipid bilayers and there is correspondingly less information known about its basic physical properties in bilayers. Specifically, the role of PE in lipid raft formation, vesicle fusion, cholesterol interactions, ion binding, and lipid flip-flop needs to be elucidated to understand its part in cell membrane function and disease pathways. To this end, my research has two goals. First, I have developed supported lipid bilayer systems that can operate with high mole percentages of PE. Second, I have begun to exploit such systems to explore the properties and functions of PE in membranes.

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Biophysical Analysis of a Successful Protocol to Reconstitute Tetramers of the M2 Muscarinic Receptor

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The human G protein-coupled receptor M2 muscarinic receptor has been functionally reconstituted in its tetrameric state into mixed lipid bilayers (Redka et al. 2013). This is achieved by first solubilizing the receptor in mixed detergent micelles composed of digitonin and sodium cholate, then reconstituting it into vesicles composed of phosphatidylcholine, phosphatidylserine and cholesterol, followed by detergent removal. To understand how the individual detergent and lipid components used in this empirical protocol contribute to the stability and activity of the receptor, we used isothermal titration calorimetry (ITC) to study the self-assembly of the mixed surfactant system; differential scanning calorimetry and pressure perturbation calorimetry to probe the phase behavior of the membrane; ITC, fluorescence (time-resolved) leakage assays and dynamic light scattering to characterize detergent-lipid interactions. The results suggest ideal mixing between digitonin and sodium cholate in the formation of mixed micelles that stabilize the receptor. Differences in membrane-partitioning behavior between the two detergents and the presence of a significant fraction of gel phase at the temperature used in the protocol contribute to non-equilibration of the detergents in the bilayer. The insights gained from this biophysical approach will aid in the mechanistic selection of detergents and conditions that influence function, oligomeric state, orientation, and accessibility of membrane proteins in future studies.

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Ion-Mobility Mass Spectrometry Assay for Incorporation of Phytanic Acid into Muscle Phospholipids

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Human dysferlinopathies (Limb-Girdle Muscular Dystrophy 2b, Myoshi Myopathy) are muscle-wasting syndromes caused by mutations in the dysferlin protein. Dysferlin loss impairs sarcolemmal repair that may contribute to disease progression. One therapeutic approach is to treat subjects with compounds that fortify the natural membrane tendency to reseal after damage, and minimize the inflammation that impedes regeneration and amplifies tissue destruction. Phytanic acid is a saturated branched chain fatty acid comprised of a 16 carbon aliphatic chain with 4 methyl groups (4ME 16:0); it is incorporated into phospholipids and triglycerides. Model phospholipid bilayers containing phytanic acid exhibit greater electrical stability than bilayers composed of straight-chain phospholipids. Phytanic acid-containing phospholipids may improve the resistance of the muscle fiber sarcolemma to stretch-induced damage. To measure phytanic acid incorporation into muscle phospholipids, dysferlin-deficient A/J mice were maintained on a defined diet supplemented with 2% phytol for three weeks; control animals received the defined diet without phytol. Muscle tissue lipids were analyzed by mass spectrometry. The muscle phosphatidylcholine species profiles were similar between phytol and control diet, except that some additional species were detected in the phytol diet muscle. The two most abundant novel species (m/z 790.7 and 862.7) are tentatively identified as PC 20:0-16:0 and PC 20:0-22:6. To confirm the presence of phytanic acid, the ion mobility of these species was compared with diphtanoyl PC standard and endogenous straight chain PC phospholipids. The ion mobility is intermediate between PC species containing either zero or two phytanic acid chains, consistent with having one phytanic acid chain. We estimate that these species represent 5% of PC. Using this methodology, we will identify phytanic acid containing species in the other classes, in order to determine the total amount of phytanic acid-containing phospholipid incorporated in the muscle.

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Fluctuation-Induced Interactions between Membrane-Bound Proteins

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The spatial organization of membrane-bound proteins is in part determined by interactions that originate from long-range correlations due to the membrane's elastic behavior. Even basic geometric mechanisms, such as the suppression of membrane height fluctuations near protein binding sites, can lead to nontrivial interactions between proteins that might result in their aggregation. To study the effect of such membrane-induced interactions, we devise a simple model that captures (a) a nonspecific repulsion between proteins, (b) elastic properties of the membrane, and (c) a local harmonic coupling between proteins and membrane shape. The model's dynamics is governed by Langevin equations to faithfully capture entropic effects and the importance of rare fluctuations. We find that the membrane induces an attractive interaction between the proteins, which aggregate to mitigate the entropic cost of suppressing membrane fluctuations. This generic mechanism might help explain the spatial patterns induced by membrane sculpting proteins.

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Effect of Phosphatidylinositol-Bisphosphate (PIP₂) Lipids on Membrane Structure and Forces

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It is widely accepted that the interaction between lipid bilayers at closest separation is dominated by a repulsive hydration force arising from the structuring of water molecules on the lipid bilayer surface. This force has been recognized as a major activation energy barrier preventing fusion of bilayers. Our working hypothesis is that the orientation of the hydrogen bond network on the bilayer surface determines the amplitude of the hydration force. We are testing this hypothesis using the 1,2-dioleoyl-*sn*-glycero-3-phospho-[1'-myo-inositol-4',5'-bisphosphate](PI(4,5)P₂) lipid and its isomers which differ in the position of phosphate groups on the inositol ring. Phosphatidylinositol-bisphosphate (PIP₂) lipids are pivotal in signaling and play an important role in exocytosis. Specifically, we have utilized small angle X-ray diffraction (SAXS) and monitored the structural consequences of osmotic pressure in multilamellar suspensions of dioleoylphosphatidylcholine (DOPC) in the presence of PI(4,5)P₂. Our preliminary data (powder X-ray diffraction and reconstructed electron density profiles) show that there are notable changes in bilayer structure, particularly the lamellar repeat distance, thickness, and forces in the presence of PI(4,5)P₂.